Amendments to the Specification

Please replace the paragraph beginning at page 17, line 10, with the following amended paragraph.

Isolated splenic macrophages were treated with lipopolysaccharide (LPS) (10ng/ml) for six hours. Extraction of mRNA was with an RNA extraction kit (Qiagen, Inc.). Then, 1μg of total mRNA was reverse transcribed in an RT mastermix (50mM KCl, 10mM Tris-HCl, 5mM $MgCl_2$, 1mM dNTP, 2.5mM oligo d(T), 50U RT, 20U RNAse inhibitor, nuclease free water-all reagents Perkin Elmer) with an initial 10 minute incubation at room temperature and then 42°C for 10 minutes. The 1μl of cDNA product was for COX-2 (sequence: 5'-GCCCACCCCAAACACAGTGCAC-3' (SEQ ID NO: 1) as a sense primer, bases 259-280, and 5'-CTCGGAACCCCCAGTCCCTACTTG-3' (SEQ ID NO: 2) as an antisense primer, bases 594-571, primer pair A); and GAPDH (sequence: 5'-CAGGAGCGACCCCACTAA-3' (SEQ ID NO: 3) as a sense primer, and 5'-GGCATCGAAGGTGGAAGAGT-3' (SEQ ID NO: 4) as an anti-sense primer). The cDNA was run on a 1% agarose gel with 3μl ethidium bromide (10mg/ml solution), and bands visualized under UV transillumination and recorded in an image acquisition processing and analysis program (Eagle Eye 2, Stratagene).

Please replace the paragraph beginning at page 24, line 29, with the following amended paragraph.

Isolated splenic macrophages were treated with LPS (10 ng/mL) for 6 hours. Extraction of mRNA was done with an RNA extraction kit (Qiagen, Inc.). Total mRNA (1 μg) was reverse transcribed in an RT mastermix (50 mM KCl, 10 mM Tris-HCl, 5 mM $MgCl_2$, 1 mM dNTP, 2.5 mM oligo d(T), 50 U RT, 20 U RNAse inhibitor, nuclease free water), (all reagents Perkin Elmer) with an initial 10 minute room temperature incubation and then 42°C for 10 minutes. The 1 μl of cDNA product was for COX-1 (sequence: 5'AGTCGAAGGAGTCTCTCGCT CTGG-3' (SEQ ID NO: 5) as a sense primer, bases 40-63, and 5'-CAGGAAATGGGTGAACGAGGGGCT-3' (SEQ ID NO: 6) as an antisense primer, bases 318-295), COX-2 (sequence: 5'-GCCCACCCCAAACACAGTGCAC-3' (SEQ ID NO: 1) as a sense primer, bases 259-280, and 5'-CTCGGAACCCCCAGTCCCTACTTG-3' (SEQ ID NO: 2) as an antisense primer, bases 594-571, primer pair A), and GAPDH (sequence: 5'-CAGGAGCGACCCCACTAA-3' (SEQ ID NO: 3) as a sense primer, and 5'-

GGCATCGAAGGTGGAAGAGT-3' (SEQ ID NO: 4) as an anti-sense primer). cDNA was run on a 1% agarose gel with 3 μL ethidium bromide (10 mg/mL solution) and bands visualized under UV transillumination and recorded in an image acquisition processing and analysis program (Eagle Eye 2, Stratagene). mRNA was quantified by RT-PCR and normalized to GAPDH.

Please replace the paragraph beginning at page 25, line 17, with the following amended paragraph.

NF-κB gel shift oligonucleotide 5' AGT TGA GGG GAC TTT CCC AGG C 3' (SEQ ID NO: 7) (Santa Cruz Laboratories, Santa Cruz, CA) was end labeled with (^{32}P) γATP using polynucleotide kinase T4 (Gibco BRL, Grand Island, NY). End labeled probe was purified from unincorporated (^{32}P)- γATP using a purification column (Bio-Rad Laboratories) and recovered in tris-EDTA buffer. Samples consisted of adherent macrophages collected after 45 minutes stimulation with 10 ng/mL LPS. Adherent cells were scraped into 1 mL of cold HANKS balanced salt solution. The cell suspension was pelleted after centrifugation in a microcentrifuge for 10 seconds and resuspended in 400 μl cold Buffer A (10 mM HEPES-KOH pH 7.9 at 4^{0}C, 1.5 mM $MgCl_2$, 10 mM KCl, 0.5 mM dithiothreitol, 0.2 mM PMSF) by agitation of the tube. The cells were allowed to swell on ice for 10 minutes, and then vortexed for 10 seconds. Samples were centrifuged for 10 seconds and the supernatant fraction was saved at -70^{0}C for IκB analysis. The pellet was resuspended in 20-100 μl of cold buffer C (20 mM HEPES-KOH pH 7.9, 25% glycerol, 420 mM NaCl, ~~1.5 mM $MgCl_2$.~~ 1.5 mM $MgCl_2$, 0.2 mM EDTA, 0.5 mM dithiothreitol, and 0.2 mM PMSF) and incubated on ice for 20 minutes. Samples were microcentrifuged for 2 minutes and supernatants collected and stored at -70^{0}C for batch analysis. Labeled probe was added to samples using standard protocols (standardized by protein), and then incubated for 20 min. Samples were subjected to electrophoretic separation on a non denaturing 5% poly-acrylamide gel at 30 mA using Tris borate EDTA for 45 minutes and analyzed by exposure to radiographic film (Kodak, Rochester, NY).

Please replace the paragraph beginning at page 33, line 8, with the following amended paragraph.

Isolated PBMC's from various groups were incubated for 18 hours at which time all groups were treated with 10 ng/mL lipopolysaccharaide (LPS) 055:B5 (Sigma, St.

Louis, MO) for 6 hours RT-PCR samples were run in a blinded fashion. Extraction of mRNA was with an RNA extraction kit (Qiagen). Total mRNA (1 μg) was reverse transcribed in an RT mastermix (50 mM KCl, 10 mM tris-HCl, 5 mM $MgCl_2$, 1 mM dNTP, 2.5 mM oligo d(T), 50 units of RT, 20 units of RNAse inhibitor, and nuclease free water; all reagents from Perkin-Elmer, Foster City, CA) with an initial 10 minute incubation at room temperature and then 42^0C for 10 minutes. The 1 μL of cDNA product was for EP1 (sense, CCA CCA CCT TCC TTC TGT TCG (SEQ ID NO: 8); anti-sense, GGT GGG CTG GCT TAG TCG TTG (SEQ ID NO: 9)); EP2 (sense, CTT ACC TGC AGC TGT ACG (SEQ ID NO: 10); anti-sense, GAT GGC AAA GAC CCA AGG (SEQ ID NO: 11)); EP3 (sense, CGC GTC AAC CAC TCC TAC ACA (SEQ ID NO: 12); anti-sense, GCA GAC CGA CAG CAC GCA CAT (SEQ ID NO: 13)); EP4 (sense, GGT CAT CTT ACT CAT TGC CAC (SEQ ID NO: 14); anti-sense, AGA TGA AGG AGC GAG AGT GG (SEQ ID NO: 15)); CD14 (sense, ACT CCC TCA ATC TGT TCG CTG (SEQ ID NO: 16); anti-sense, CTG AAG CCA AGG CAG TTT GAG TCC (SEQ ID NO: 17)); COX-2 (sequence: sense GCC CAC CCC AAA CAC AGT GCA C (SEQ ID NO: 18), bases 259-280; antisense CTC GGA ACC CCC AGT CCC TAC TTG (SEQ ID NO: 19), bases 594-571); and GAPDH (sequence: sense CAG GAG CGA CCC CAC TAA (SEQ ID NO: 20); anti-GGC ATC GAA GGT GGA AGA GT (SEQ ID NO: 21)). The cDNA was run on a 1% agarose gel with 3 μL of ethidium bromide (10 mg/mL solution) and bands were visualized under UV transillumination and recorded in an image acquisition processing and analysis program (Eagle Eye 2, Stratagene).